

SEQUENCE LISTING

<110> Hammer, Philip E.
Hinson, Todd K.
Carr, Brian
Duck, Nicholas B.

<120> GDC-1 GENES CONFERRING HERBICIDE
RESISTANCE

<130> 045600/275114

<150> 60/453,237

<151> 2003-03-10

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<170> FastSEQ for Windows Version 4.0

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<222> (224)...(1951)

<223> Fungal isolate from soil sample

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Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe	
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Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu	
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<223> Fungal isolate from soil sample

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Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	
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Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	
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Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	
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Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	
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<223> Fungal isolate from soil sample

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Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys
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ccc atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc 335
Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe
      100                105                110

att cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc 383
Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe
      115                120                125

aag gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc 431
Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe
      130                135                140

gcc gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc 479
Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr
      145                150                155

ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa 527
Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys
      160                165                170                175

gaa gat gct cct cga gca ttg atc atg act gca gaa gct agc gcg agg 575
Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg
      180                185                190

aac aat gcc aag aca gag taa agtggactgt catgaaggcc gatttaccac 626
Asn Asn Ala Lys Thr Glu *
      195

ctcataaatt gtaatagacc tgatacacat agatcaaggc aggtaccgat cattaatcaa 686
gcagggtttgg atgggggaagg attttgaaaa tgaggaaacg atgggatgat atttggaata 746
actggccatt attttgagta cttataaaca aatttgaagt tcaatttttt ttcaaaaaaaaa 806
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 835

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<210> 5
<211> 591
<212> DNA
<213> Unknown

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<220>
<221> CDS
<222> (1)...(591)

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<223> Fungal isolate from soil sample

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<400> 5

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Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val	
1 5 10 15	
att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt	96
Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe	
20 25 30	
ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt	144
Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly	
35 40 45	
tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac	192
Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp	
50 55 60	
aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag	240
Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln	
65 70 75 80	
ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc	288
Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro	
85 90 95	
atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att	336
Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile	
100 105 110	
cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag	384
His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys	
115 120 125	
gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc	432
Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala	
130 135 140	
gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt	480
Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe	
145 150 155 160	
aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa	528
Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu	
165 170 175	
gat gct cct cga gca ttg atc atg act gca gaa gct agc gcg agg aac	576
Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg Asn	
180 185 190	
aat gcc aag aca gag	591
Asn Ala Lys Thr Glu	
195	

<210> 6
 <211> 197
 <212> PRT

<213> Unknown

<220>

<223> Fungal isolate from soil sample

<400> 6

Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val
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Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe
		20					25					30			
Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly
	35					40					45				
Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu	Ala	Ala	Ala	Asp	Asp
50					55				60						
Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	Gln
65				70					75					80	
Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro
		85						90					95		
Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile
		100					105					110			
His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys
	115						120					125			
Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala
130					135				140						
Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe
145				150					155					160	
Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu
		165						170					175		
Asp	Ala	Pro	Arg	Ala	Leu	Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	Asn
		180					185					190			
Asn	Ala	Lys	Thr	Glu											
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<210> 7

<211> 678

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(678)

<223> Fungal isolate from soil sample

<400> 7

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Thr	Tyr	Pro	Gly	Val	Gln	Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	
1			5					10					15			
cag	ctc	gat	gca	tct	gag	atc	aac	gct	cag	cca	gcg	cca	gtc	gtc	gag	96
Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	
		20					25					30				
aat	gaa	gtt	gcc	aaa	aac	cga	gat	aac	tca	ccc	gtc	att	aca	caa	gct	144
Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	
	35						40					45				

ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag aag aac gac atc gtc	192
Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val	
50 55 60	
att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt	240
Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe	
65 70 75 80	
ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt	288
Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly	
85 90 95	
tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac	336
Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp	
100 105 110	
aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag	384
Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln	
115 120 125	
ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc	432
Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro	
130 135 140	
atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att	480
Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile	
145 150 155 160	
cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag	528
His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys	
165 170 175	
gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc	576
Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala	
180 185 190	
gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt	624
Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe	
195 200 205	
aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa	672
Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu	
210 215 220	
gat gct	678
Asp Ala	
225	

<210> 8

<211> 226

<212> PRT

<213> Unknown

<220>

<223> Fungal isolate from soil sample

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 20 25 30
 Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro Val Ile Thr Gln Ala
 35 40 45
 Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val
 50 55 60
 Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe
 65 70 75 80
 Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly
 85 90 95
 Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp
 100 105 110
 Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln
 115 120 125
 Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro
 130 135 140
 Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile
 145 150 155 160
 His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys
 165 170 175
 Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala
 180 185 190
 Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe
 195 200 205
 Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu
 210 215 220
 Asp Ala
 225

<210> 9
 <211> 1636
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1377)

<223> Fungal isolate from soil sample

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 1 5 10 15
 atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag ctc 96
 Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu
 20 25 30
 acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc gtt 144
 Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val
 35 40 45

tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg	192
Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met	
50 55 60	
gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg	240
Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu	
65 70 75 80	
tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt	288
Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val	
85 90 95	
gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat	336
Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp	
100 105 110	
gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc	384
Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile	
115 120 125	
gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct	432
Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala	
130 135 140	
gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac ggc	480
Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly	
145 150 155 160	
tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata	528
Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile	
165 170 175	
ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc tct	576
Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser	
180 185 190	
tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac tgc	624
Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys	
195 200 205	
att gtc aaa tac tcg aca tat cca ggt gtc cag atg agg ggt gtg ctg	672
Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu	
210 215 220	
cga caa gtg att aag cag ctc gat gca tct gag atc aac gct cag cca	720
Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro	
225 230 235 240	
gcg cca gtc gtc gag aat gaa gtt gcc aaa aac cga gat aac tca ccc	768
Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro	
245 250 255	
gtc att aca caa gct ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag	816
Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys	
260 265 270	

aag aac gac atc gtc att acc gag act gga aca gcc aac ttt ggc atc	864
Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile	
275 280 285	
tgg gat act aag ttt ccc tct ggc gtt act gcg ctt tct cag gtc ctt	912
Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu	
290 295 300	
tgg gga agc att ggt tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt	960
Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu	
305 310 315 320	
gca gcc gcc gat gac aac agc gat cgc aga act atc ctc ttt gtt ggt	1008
Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly	
325 330 335	
gat ggc tca ttc cag ctc act gct caa gaa ttg agc aca atg att cgt	1056
Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg	
340 345 350	
ctc aag ctg aag ccc atc atc ttt gtc atc tgc aac gat ggc ttt acc	1104
Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr	
355 360 365	
att gaa cga ttc att cac ggc atg gaa gcc gag tac aac gac atc gca	1152
Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala	
370 375 380	
aat tgg gac ttc aag gct ctg gtt gac gtc ttt ggc ggc tct aag acg	1200
Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr	
385 390 395 400	
gcc aag aag ttc gcc gtc aag acc aag gac gag ctg gac agc ctt ctc	1248
Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu	
405 410 415	
aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta	1296
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu	
420 425 430	
tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca gaa	1344
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu	
435 440 445	
gct agc gcg agg aac aat gcc aag aca gag taa agtggactgt catgaaggcc	1397
Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *	
450 455	
gatttaccac ctcataaatt gtaatagacc tgatacacat agatcaaggc aggtaccgat	1457
cattaatcaa gcaggtttgg atggggaagg attttgaaaa tgaggaaacg atgggatgat	1517
atttggaata actggccatt attttgagta cttataaaca aatttgaagt tcaatttttt	1577
ttcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1636

<210> 10
 <211> 1374
 <212> DNA
 <213> Unknown

<220>

<221> CDS

<222> (1)...(1374)

<223> Fungal isolate from soil sample

<400> 10

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1 5 10 15	
atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag ctc	96
Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu	
20 25 30	
acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc gtt	144
Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val	
35 40 45	
tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg	192
Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met	
50 55 60	
gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg	240
Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu	
65 70 75 80	
tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt	288
Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val	
85 90 95	
gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat	336
Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp	
100 105 110	
gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc	384
Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile	
115 120 125	
gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct	432
Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala	
130 135 140	
gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac ggc	480
Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly	
145 150 155 160	
tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata	528
Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile	
165 170 175	
ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc tct	576
Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser	
180 185 190	
tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac tgc	624

Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu	His	Ser	Asp	His	Cys	
		195					200					205				
att	gtc	aaa	tac	tcg	aca	tat	cca	ggg	gtc	cag	atg	agg	ggg	gtg	ctg	672
Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln	Met	Arg	Gly	Val	Leu	
	210					215					220					
cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	atc	aac	gct	cag	cca	720
Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln	Pro	
	225				230					235					240	
gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	cga	gat	aac	tca	ccc	768
Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro	
				245				250						255		
gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	gga	gag	ttc	ctg	aag	816
Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys	
		260					265					270				
aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	gcc	aac	ttt	ggc	atc	864
Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile	
	275					280					285					
tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	ctt	tct	cag	gtc	ctt	912
Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu	
	290				295						300					
tgg	gga	agc	att	ggg	tgg	tcc	gtt	ggg	gcc	tgc	caa	gga	gcc	gtt	ctt	960
Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu	
	305				310					315					320	
gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	atc	ctc	ttt	gtt	ggg	1008
Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly	
				325				330						335		
gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	agc	aca	atg	att	cgt	1056
Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg	
		340					345					350				
ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	aac	gat	ggc	ttt	acc	1104
Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr	
	355					360						365				
att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	tac	aac	gac	atc	gca	1152
Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala	
	370					375					380					
aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	ggc	ggc	tct	aag	acg	1200
Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr	
	385				390					395					400	
gcc	aag	aag	ttc	gcc	gtc	aag	acc	aag	gac	gag	ctg	gac	agc	ctt	ctc	1248
Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu	
				405				410						415		
aca	gac	cct	acc	ttt	aac	gcc	gca	gaa	tgc	ctc	cag	ttt	gtc	gag	cta	1296
Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu	

420	425	430	
tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca gaa			1344
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu			
435	440	445	

450	455		1374
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Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu			

<210> 11
 <211> 458
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 11

Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn			
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Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu			
20 25 30			
Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val			
35 40 45			
Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met			
50 55 60			
Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu			
65 70 75 80			
Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val			
85 90 95			
Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp			
100 105 110			
Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile			
115 120 125			
Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala			
130 135 140			
Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly			
145 150 155 160			
Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile			
165 170 175			
Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser			
180 185 190			
Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys			
195 200 205			
Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu			
210 215 220			
Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro			
225 230 235 240			
Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro			
245 250 255			
Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys			
260 265 270			
Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile			
275 280 285			
Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu			

290		295		300
Trp Gly Ser Ile Gly	Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu			
305	310	315	320	
Ala Ala Ala Asp Asp	Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly			
	325	330	335	
Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg				
	340	345	350	
Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr				
	355	360	365	
Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala				
	370	375	380	
Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr				
385	390	395	400	
Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu				
	405	410	415	
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu				
	420	425	430	
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu				
	435	440	445	
Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu				
450	455			

<210> 12
 <211> 30
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(30)

<223> Oligonucleotide used for PCR amplification of
 GDC-1

<400> 12
 tcc cag atg cca aag ttg gct gtt cca gtc
 Ser Gln Met Pro Lys Leu Ala Val Pro Val
 1 5 10

30

<210> 13
 <211> 563
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 13
 Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln
 1 5 10 15
 Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
 20 25 30
 Leu Leu Asp Lys Ile Tyr Glu Val Gly Met Arg Trp Ala Gly Asn
 35 40 45
 Ala Asn Glu Leu Asn Ala Arg Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
 50 55 60
 Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
 65 70 75 80

Ala	Leu	Asn	Gly	Ile	Ala	Gly	Ser	Tyr	Ala	Glu	His	Val	Gly	Val	Leu	
				85					90					95		
His	Val	Val	Gly	Val	Pro	Ser	Ile	Ser	Ser	Gln	Ala	Lys	Gln	Leu	Leu	
			100					105					110			
Leu	His	His	Thr	Leu	Gly	Asn	Gly	Asp	Phe	Thr	Val	Phe	His	Arg	Met	
		115					120					125				
Ser	Ala	Asn	Ile	Ser	Glu	Thr	Thr	Ala	Met	Ile	Thr	Asp	Ile	Cys	Thr	
	130						135					140				
Ala	Pro	Ala	Glu	Ile	Asp	Arg	Cys	Ile	Arg	Thr	Tyr	Val	Thr	Gln		
145					150						155			160		
Arg	Pro	Val	Tyr	Leu	Gly	Leu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Asn	Val	
			165						170					175		
Pro	Ala	Lys	Leu	Leu	Gln	Thr	Pro	Ile	Asp	Met	Ser	Leu	Lys	Pro	Asn	
			180						185					190		
Asp	Ala	Glu	Ser	Glu	Lys	Glu	Val	Ile	Asp	Thr	Ile	Leu	Val	Leu	Ala	
		195						200				205				
Lys	Asp	Ala	Lys	Asn	Pro	Val	Ile	Leu	Ala	Asp	Ala	Cys	Cys	Ser	Arg	
	210						215					220				
His	Asp	Val	Lys	Ala	Glu	Thr	Lys	Lys	Leu	Ile	Asp	Leu	Thr	Gln	Phe	
225					230						235			240		
Pro	Ala	Phe	Val	Thr	Pro	Met	Gly	Lys	Gly	Ser	Ile	Ser	Glu	Gln	His	
			245						250					255		
Pro	Arg	Tyr	Gly	Gly	Val	Tyr	Val	Gly	Thr	Leu	Ser	Lys	Pro	Glu	Val	
			260					265						270		
Lys	Glu	Ala	Val	Glu	Ser	Ala	Asp	Leu	Ile	Leu	Ser	Val	Gly	Ala	Leu	
		275					280						285			
Leu	Ser	Asp	Phe	Asn	Thr	Gly	Ser	Phe	Ser	Tyr	Ser	Tyr	Lys	Thr	Lys	
	290						295					300				
Asn	Ile	Val	Glu	Phe	His	Ser	Asp	His	Met	Lys	Ile	Arg	Asn	Ala	Thr	
305					310						315				320	
Phe	Pro	Gly	Val	Gln	Met	Lys	Phe	Val	Leu	Gln	Lys	Leu	Leu	Thr	Asn	
			325						330					335		
Ile	Ala	Asp	Ala	Ala	Lys	Gly	Tyr	Lys	Pro	Val	Ala	Val	Pro	Ala	Arg	
			340					345						350		
Thr	Pro	Ala	Asn	Ala	Ala	Val	Pro	Ala	Ser	Thr	Pro	Leu	Lys	Gln	Glu	
		355						360					365			
Trp	Met	Trp	Asn	Gln	Leu	Gly	Asn	Phe	Leu	Gln	Glu	Gly	Asp	Val	Val	
	370						375					380				
Ile	Ala	Glu	Thr	Gly	Thr	Ser	Ala	Phe	Gly	Ile	Asn	Gln	Thr	Thr	Phe	
385					390						395			400		
Pro	Asn	Asn	Thr	Tyr	Gly	Ile	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	
			405						410					415		
Phe	Thr	Thr	Gly	Ala	Thr	Leu	Gly	Ala	Ala	Phe	Ala	Ala	Glu	Glu	Ile	
			420					425					430			
Asp	Pro	Lys	Lys	Arg	Val	Ile	Leu	Phe	Ile	Gly	Asp	Gly	Ser	Leu	Gln	
		435					440					445				
Leu	Thr	Val	Gln	Glu	Ile	Ser	Thr	Met	Ile	Arg	Trp	Gly	Leu	Lys	Pro	
	450						455					460				
Tyr	Leu	Phe	Val	Leu	Asn	Asp	Gly	Tyr	Thr	Ile	Glu	Lys	Leu	Ile		
465					470					475				480		
His	Gly	Pro	Lys	Ala	Gln	Tyr	Asn	Glu	Ile	Gln	Gly	Trp	Asp	His	Leu	
			485						490					495		
Ser	Leu	Leu	Pro	Thr	Phe	Gly	Ala	Lys	Asp	Tyr	Glu	Thr	His	Arg	Val	
			500					505					510			
Ala	Thr	Thr	Gly	Glu	Trp	Asp	Lys	Leu	Thr	Gln	Asp	Lys	Ser	Phe	Asn	
		515					520					525				
Asp	Asn	Ser	Lys	Ile	Arg	Met	Ile	Glu	Val	Met	Leu	Pro	Val	Phe	Asp	

530		535		540
Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn				
545		550		555
Ala Lys Gln				560

<210> 14
 <211> 550
 <212> PRT
 <213> Salmonella typhimurium

<400> 14

Met	Gln	Asn	Pro	Tyr	Thr	Val	Ala	Asp	Tyr	Leu	Leu	Asp	Arg	Leu	Ala
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Gly	Cys	Gly	Ile	Gly	His	Leu	Phe	Gly	Val	Pro	Gly	Asp	Tyr	Asn	Leu
		20						25					30		
Gln	Phe	Leu	Asp	His	Val	Ile	Asp	His	Pro	Thr	Leu	Arg	Trp	Val	Gly
		35					40					45			
Cys	Ala	Asn	Glu	Leu	Asn	Ala	Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg
	50					55					60				
Met	Ser	Gly	Ala	Gly	Ala	Leu	Leu	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu
65					70					75				80	
Ser	Ala	Ile	Asn	Gly	Ile	Ala	Gly	Ser	Tyr	Ala	Glu	Tyr	Val	Pro	Val
			85					90						95	
Leu	His	Ile	Val	Gly	Ala	Pro	Cys	Ser	Ala	Ala	Gln	Gln	Arg	Gly	Glu
		100						105						110	
Leu	Met	His	His	Thr	Leu	Gly	Asp	Gly	Asp	Phe	Arg	His	Phe	Tyr	Arg
		115					120					125			
Met	Ser	Gln	Ala	Ile	Ser	Ala	Ala	Ser	Ala	Ile	Leu	Asp	Glu	Gln	Asn
	130					135					140				
Ala	Cys	Phe	Glu	Ile	Asp	Arg	Val	Leu	Gly	Glu	Met	Leu	Ala	Ala	Arg
145					150					155					160
Arg	Pro	Gly	Tyr	Ile	Met	Leu	Pro	Ala	Asp	Val	Ala	Lys	Lys	Thr	Ala
				165					170					175	
Ile	Pro	Pro	Thr	Gln	Ala	Leu	Ala	Leu	Pro	Val	His	Glu	Ala	Gln	Ser
			180					185						190	
Gly	Val	Glu	Thr	Ala	Phe	Arg	Tyr	His	Ala	Arg	Gln	Cys	Leu	Met	Asn
		195					200					205			
Ser	Arg	Arg	Ile	Ala	Leu	Leu	Ala	Asp	Phe	Leu	Ala	Gly	Arg	Phe	Gly
	210					215					220				
Leu	Arg	Pro	Leu	Leu	Gln	Arg	Trp	Met	Ala	Glu	Thr	Pro	Ile	Ala	His
225					230					235				240	
Ala	Thr	Leu	Leu	Met	Gly	Lys	Gly	Leu	Phe	Asp	Glu	Gln	His	Pro	Asn
			245						250					255	
Phe	Val	Gly	Thr	Tyr	Ser	Ala	Gly	Ala	Ser	Ser	Lys	Glu	Val	Arg	Gln
		260						265						270	
Ala	Ile	Glu	Asp	Ala	Asp	Arg	Val	Ile	Cys	Val	Gly	Thr	Arg	Phe	Val
	275						280					285			
Asp	Thr	Leu	Thr	Ala	Gly	Phe	Thr	Gln	Gln	Leu	Pro	Ala	Glu	Arg	Thr
	290					295					300				
Leu	Glu	Ile	Gln	Pro	Tyr	Ala	Ser	Arg	Ile	Gly	Glu	Thr	Trp	Phe	Asn
305					310					315				320	
Leu	Pro	Met	Ala	Gln	Ala	Val	Ser	Thr	Leu	Arg	Glu	Leu	Cys	Leu	Glu
			325						330					335	
Cys	Ala	Phe	Ala	Pro	Pro	Pro	Thr	Arg	Ser	Ala	Gly	Gln	Pro	Val	Arg
			340					345					350		

Ile	Asp	Lys	Gly	Glu	Leu	Thr	Gln	Glu	Ser	Phe	Trp	Gln	Thr	Leu	Gln
	355						360					365			
Gln	Tyr	Leu	Lys	Pro	Gly	Asp	Ile	Ile	Leu	Val	Asp	Gln	Gly	Thr	Ala
	370					375					380				
Ala	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Leu	Pro	Asp	Gly	Ala	Glu	Val	Val
385					390					395					400
Leu	Gln	Pro	Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Ser	Leu	Pro	Ala	Ala	Phe
			405					410						415	
Gly	Ala	Gln	Thr	Ala	Cys	Pro	Asp	Arg	Arg	Val	Ile	Leu	Ile	Ile	Gly
		420					425						430		
Asp	Gly	Ala	Ala	Gln	Leu	Thr	Ile	Gln	Glu	Met	Gly	Ser	Met	Leu	Arg
	435						440					445			
Asp	Gly	Gln	Ala	Pro	Val	Ile	Leu	Leu	Leu	Asn	Asn	Asp	Gly	Tyr	Thr
	450					455					460				
Val	Glu	Arg	Ala	Ile	His	Gly	Ala	Ala	Gln	Arg	Tyr	Asn	Asp	Ile	Ala
465				470					475						480
Ser	Trp	Asn	Trp	Thr	Gln	Ile	Pro	Pro	Ala	Leu	Asn	Ala	Ala	Gln	Gln
			485					490						495	
Ala	Glu	Cys	Trp	Arg	Val	Thr	Gln	Ala	Ile	Gln	Leu	Ala	Glu	Val	Leu
		500					505					510			
Glu	Arg	Leu	Ala	Arg	Pro	Gln	Arg	Leu	Ser	Phe	Ile	Glu	Val	Met	Leu
	515					520						525			
Pro	Lys	Ala	Asp	Leu	Pro	Glu	Leu	Leu	Arg	Thr	Val	Thr	Arg	Ala	Leu
	530					535					540				
Glu	Ala	Arg	Asn	Gly	Gly										
545					550										

<210> 15
 <211> 568
 <212> PRT
 <213> Zymomonas mobilis

<400> 15															
Met	Ser	Tyr	Thr	Val	Gly	Thr	Tyr	Leu	Ala	Glu	Arg	Leu	Val	Gln	Ile
1				5					10					15	
Gly	Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu
			20					25					30		
Leu	Asp	Asn	Leu	Leu	Leu	Asn	Lys	Asn	Met	Glu	Gln	Val	Tyr	Cys	Cys
	35					40						45			
Asn	Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Lys
	50				55						60				
Gly	Ala	Ala	Ala	Ala	Val	Val	Thr	Tyr	Ser	Val	Gly	Ala	His	Ser	Ala
65				70						75				80	
Phe	Asp	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu
			85					90						95	
Ile	Ser	Gly	Ala	Pro	Asn	Asn	Asn	Asp	His	Ala	Ala	Gly	His	Val	Leu
		100					105						110		
His	His	Ala	Leu	Gly	Lys	Thr	Asp	Tyr	His	Tyr	Gln	Leu	Glu	Met	Ala
	115					120					125				
Lys	Asn	Ile	Thr	Ala	Ala	Ala	Glu	Ala	Ile	Tyr	Thr	Pro	Glu	Glu	Ala
	130					135					140				
Pro	Ala	Lys	Ile	Asp	His	Val	Ile	Lys	Thr	Ala	Leu	Ala	Lys	Lys	Lys
145				150						155				160	
Pro	Val	Tyr	Leu	Glu	Ile	Ala	Cys	Asn	Ile	Ala	Ser	Met	Pro	Cys	Ala
			165					170						175	
Ala	Pro	Gly	Pro	Ala	Ser	Ala	Leu	Phe	Asn	Asp	Glu	Ala	Ser	Asp	Glu

			180					185					190				
Ala	Ser	Leu	Asn	Ala	Ala	Val	Asp	Glu	Thr	Leu	Lys	Phe	Ile	Ala	Asn		
		195					200					205					
Arg	Asp	Lys	Val	Ala	Val	Leu	Val	Gly	Ser	Lys	Leu	Arg	Ala	Ala	Gly		
	210					215					220						
Ala	Glu	Glu	Ala	Ala	Val	Lys	Phe	Thr	Asp	Ala	Leu	Gly	Gly	Ala	Val		
225					230					235					240		
Ala	Thr	Met	Ala	Ala	Ala	Lys	Ser	Phe	Phe	Pro	Glu	Glu	Asn	Pro	His		
			245						250					255			
Tyr	Ile	Gly	Thr	Ser	Trp	Gly	Glu	Val	Ser	Tyr	Pro	Gly	Val	Glu	Lys		
		260						265					270				
Thr	Met	Lys	Glu	Ala	Asp	Ala	Val	Ile	Ala	Leu	Ala	Pro	Val	Phe	Asn		
	275						280					285					
Asp	Tyr	Ser	Thr	Thr	Gly	Trp	Thr	Asp	Ile	Pro	Asp	Pro	Lys	Lys	Leu		
	290				295						300						
Val	Leu	Ala	Glu	Pro	Arg	Ser	Val	Val	Val	Arg	Arg	Ile	Arg	Phe	Pro		
305					310					315					320		
Ser	Val	His	Leu	Lys	Asp	Tyr	Leu	Thr	Arg	Leu	Ala	Gln	Lys	Val	Ser		
			325						330					335			
Lys	Lys	Thr	Gly	Ser	Leu	Asp	Phe	Phe	Lys	Ser	Leu	Asn	Ala	Gly	Glu		
		340						345					350				
Leu	Lys	Lys	Ala	Ala	Pro	Ala	Asp	Pro	Ser	Ala	Pro	Leu	Val	Asn	Ala		
	355					360						365					
Glu	Ile	Ala	Arg	Gln	Val	Glu	Ala	Leu	Leu	Thr	Pro	Asn	Thr	Thr	Val		
	370					375					380						
Ile	Ala	Glu	Thr	Gly	Asp	Ser	Trp	Phe	Asn	Ala	Gln	Arg	Met	Lys	Leu		
385					390					395				400			
Pro	Asn	Gly	Ala	Arg	Val	Glu	Tyr	Glu	Met	Gln	Trp	Gly	His	Ile	Gly		
			405						410					415			
Trp	Ser	Val	Pro	Ala	Ala	Phe	Gly	Tyr	Ala	Val	Gly	Ala	Pro	Glu	Arg		
		420						425					430				
Arg	Asn	Ile	Leu	Met	Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln		
	435						440					445					
Glu	Val	Ala	Gln	Met	Val	Arg	Leu	Lys	Leu	Pro	Val	Ile	Ile	Phe	Leu		
	450					455					460						
Ile	Asn	Asn	Tyr	Gly	Tyr	Thr	Ile	Glu	Val	Met	Ile	His	Asp	Gly	Pro		
465					470					475					480		
Tyr	Asn	Asn	Ile	Lys	Asn	Trp	Asp	Tyr	Ala	Gly	Leu	Met	Glu	Val	Phe		
			485					490					495				
Asn	Gly	Asn	Gly	Gly	Tyr	Asp	Ser	Gly	Ala	Ala	Lys	Gly	Leu	Lys	Ala		
		500						505					510				
Lys	Thr	Gly	Gly	Glu	Leu	Ala	Glu	Ala	Ile	Lys	Val	Ala	Leu	Ala	Asn		
	515						520					525					
Thr	Asp	Gly	Pro	Thr	Leu	Ile	Glu	Cys	Phe	Ile	Gly	Arg	Glu	Asp	Cys		
	530					535					540						
Thr	Glu	Glu	Leu	Val	Lys	Trp	Gly	Lys	Arg	Val	Ala	Ala	Ala	Asn	Ser		
545					550					555					560		
Arg	Lys	Pro	Val	Asn	Lys	Leu	Leu										
			565														

<210> 16

<211> 687

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

RTA01/2151347v1

450		455		460
Glu Thr Pro Gly Ser Lys Ile Lys Pro Gln Thr Val Ile Lys Lys Leu				
465		470		475
Ser Lys Val Ala Asn Asp Thr Gly Arg His Val Ile Val Thr Thr Gly				480
		485		490
Val Gly Gln His Gln Met Trp Ala Ala Gln His Trp Thr Trp Arg Asn				495
		500		505
Pro His Thr Phe Ile Thr Ser Gly Gly Leu Gly Thr Met Gly Tyr Gly				510
		515		520
Leu Pro Ala Ala Ile Gly Ala Gln Val Ala Lys Pro Glu Ser Leu Val				525
		530		535
Ile Asp Ile Asp Gly Asp Ala Ser Phe Asn Met Thr Leu Thr Glu Leu				540
545		550		555
Ser Ser Ala Val Gln Ala Gly Thr Pro Val Lys Ile Leu Ile Leu Asn				560
		565		570
Asn Glu Glu Gln Gly Met Val Thr Gln Trp Gln Ser Leu Phe Tyr Glu				575
		580		585
His Arg Tyr Ser His Thr His Gln Leu Asn Pro Asp Phe Ile Lys Leu				590
		595		600
Ala Glu Ala Met Gly Leu Lys Gly Leu Arg Val Lys Lys Gln Glu Glu				605
		610		615
Leu Asp Ala Lys Leu Lys Glu Phe Val Ser Thr Lys Gly Pro Val Leu				620
625		630		635
Leu Glu Val Glu Val Asp Lys Lys Val Pro Val Leu Pro Met Val Ala				640
		645		650
Gly Gly Ser Gly Leu Asp Glu Phe Ile Asn Phe Asp Pro Glu Val Glu				655
		660		665
Arg Gln Gln Thr Glu Leu Arg His Lys Arg Thr Gly Gly Lys His				670
		675		680
				685

<210> 17

<211> 686

<212> PRT

<213> Magnaporthe grisea

<400> 17

Met Leu Arg Thr Val Gly Arg Lys Ala Leu Arg Gly Ser Ser Lys Gly				
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Cys Ser Arg Thr Ile Ser Thr Leu Lys Pro Ala Thr Ala Thr Ile Ala				15
		20		25
Lys Pro Gly Ser Arg Thr Leu Ser Thr Pro Ala Thr Ala Thr Ala Thr				30
		35		40
Ala Pro Arg Thr Lys Pro Ser Ala Ser Phe Asn Ala Arg Arg Asp Pro				45
		50		55
Gln Pro Leu Val Asn Pro Arg Ser Gly Glu Ala Asp Glu Ser Phe Ile				60
65		70		75
Gly Lys Thr Gly Gly Glu Ile Phe His Glu Met Met Leu Arg Gln Asn				80
		85		90
Val Lys His Ile Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe				95
		100		105
Asp Ala Ile Tyr Asn Ser Lys His Ile Asp Phe Val Leu Pro Lys His				110
		115		120
Glu Gln Gly Ala Gly His Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly				125
		130		135
Lys Pro Gly Val Val Leu Val Thr Ser Gly Pro Gly Ala Thr Asn Val				140
145		150		155
				160

Ile	Thr	Pro	Met	Ala	Asp	Ala	Leu	Ala	Asp	Gly	Thr	Pro	Leu	Val	Val	
				165					170					175		
Phe	Ser	Gly	Gln	Val	Val	Thr	Ser	Asp	Ile	Gly	Ser	Asp	Ala	Phe	Gln	
			180					185					190			
Glu	Ala	Asp	Val	Ile	Gly	Ile	Ser	Arg	Ser	Cys	Thr	Lys	Trp	Asn	Val	
		195					200					205				
Met	Val	Lys	Ser	Ala	Asp	Glu	Leu	Pro	Arg	Arg	Ile	Asn	Glu	Ala	Phe	
	210				215						220					
Glu	Ile	Ala	Thr	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Pro	Ala	
225					230					235					240	
Lys	Asp	Val	Thr	Ala	Ser	Val	Leu	Arg	Arg	Ala	Ile	Pro	Thr	Glu	Thr	
			245					250						255		
Ser	Ile	Pro	Ser	Ile	Ser	Ala	Ala	Ala	Arg	Ala	Val	Gln	Glu	Ala	Gly	
		260					265						270			
Arg	Lys	Gln	Leu	Glu	His	Ser	Ile	Lys	Arg	Val	Ala	Asp	Leu	Val	Asn	
		275					280					285				
Ile	Ala	Lys	Lys	Pro	Val	Ile	Tyr	Ala	Gly	Gln	Gly	Val	Ile	Leu	Ser	
	290					295					300					
Glu	Gly	Gly	Val	Glu	Leu	Leu	Lys	Ala	Leu	Ala	Asp	Lys	Ala	Ser	Ile	
305					310					315					320	
Pro	Val	Thr	Thr	Thr	Leu	His	Gly	Leu	Gly	Ala	Phe	Asp	Glu	Leu	Asp	
			325					330						335		
Glu	Lys	Ala	Leu	His	Met	Leu	Gly	Met	His	Gly	Ser	Ala	Tyr	Ala	Asn	
		340					345					350				
Met	Ser	Met	Gln	Glu	Ala	Asp	Leu	Ile	Ile	Ala	Leu	Gly	Gly	Arg	Phe	
		355				360						365				
Asp	Asp	Arg	Val	Thr	Gly	Ser	Ile	Pro	Lys	Phe	Ala	Pro	Ala	Ala	Lys	
	370				375						380					
Leu	Ala	Ala	Ala	Glu	Gly	Arg	Gly	Gly	Ile	Val	His	Phe	Glu	Ile	Met	
385					390					395					400	
Pro	Lys	Asn	Ile	Asn	Lys	Val	Val	Gln	Ala	Thr	Glu	Ala	Ile	Glu	Gly	
			405					410						415		
Asp	Val	Ala	Ser	Asn	Leu	Lys	Leu	Leu	Pro	Lys	Ile	Glu	Gln	Arg		
		420					425					430				
Ser	Met	Thr	Asp	Arg	Lys	Glu	Trp	Phe	Asp	Gln	Ile	Lys	Glu	Trp	Lys	
		435				440						445				
Glu	Lys	Trp	Pro	Leu	Ser	His	Tyr	Glu	Arg	Ala	Glu	Arg	Ser	Gly	Leu	
	450					455					460					
Ile	Lys	Pro	Gln	Thr	Leu	Ile	Glu	Glu	Leu	Ser	Asn	Leu	Thr	Ala	Asp	
465					470					475					480	
Arg	Lys	Asp	Met	Thr	Tyr	Ile	Thr	Thr	Gly	Val	Gly	Gln	His	Gln	Met	
			485					490						495		
Trp	Thr	Ala	Gln	His	Phe	Arg	Trp	Arg	His	Pro	Arg	Ser	Met	Ile	Thr	
		500					505					510				
Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Gly	Leu	Pro	Ala	Ala	Ile	Gly	
	515					520						525				
Ala	Lys	Val	Ala	Arg	Pro	Asp	Ala	Leu	Val	Ile	Asp	Ile	Asp	Gly	Asp	
	530					535					540					
Ala	Ser	Phe	Asn	Met	Thr	Leu	Thr	Glu	Leu	Ser	Thr	Ala	Ala	Gln	Phe	
545					550					555					560	
Asn	Ile	Gly	Val	Lys	Val	Ile	Val	Leu	Asn	Asn	Glu	Glu	Gln	Gly	Met	
			565					570						575		
Val	Thr	Gln	Trp	Gln	Asn	Leu	Phe	Tyr	Glu	Asp	Arg	Tyr	Ser	His	Thr	
		580						585					590			
His	Gln	Arg	Asn	Pro	Asp	Phe	Met	Lys	Leu	Ala	Asp	Ala	Met	Asp	Val	
	595					600					605					
Gln	His	Arg	Arg	Val	Ser	Lys	Pro	Asp	Asp	Val	Gly	Asp	Ala	Leu	Thr	

610		615		620
Trp Leu Ile Asn Thr Asp Gly Pro Ala Leu Leu Glu Val Met Thr Asp				
625		630		635
Lys Lys Val Pro Val Leu Pro Met Val Pro Gly Gly Asn Gly Leu His				
	645		650	655
Glu Phe Ile Thr Phe Asp Ala Ser Lys Asp Lys Gln Arg Arg Glu Leu				
	660		665	670
Met Arg Ala Arg Thr Asn Gly Leu His Gly Arg Thr Ala Val				
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<210> 18

<211> 1728

<212> DNA

<213> Unknown

<220>

<223> Fungal isolate from soil sample

<221> CDS

<222> (1)...(1728)

<400> 18

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1 5 10 15	
ggt gcc gag tat ctt ttc cgg cgt ctc cac gaa atc ggc att cgc tcc	96
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser	
20 25 30	
atc cac ggt ctt cca ggc gat tac aac cct ctt gcc ctc gac tat ttg	144
Ile His Gly Leu Pro Gly Asp Tyr Asn Pro Leu Ala Leu Asp Tyr Leu	
35 40 45	
cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct	192
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala	
50 55 60	
gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc	240
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu	
65 70 75 80	
atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc	288
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala	
85 90 95	
ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct	336
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro	
100 105 110	
tcc act gcc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga	384
Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly	
115 120 125	
aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc	432
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys	

130	135	140	
gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp 145 150 155 160			480
cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met 165 170 175			528
ctt ccc acc gat atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys 180 185 190			576
gaa cca att gac ttg tcg gag cct cca aat gat ccc gag aaa gaa gca Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala 195 200 205			624
tac gtc gtt gac gtt gtc ctc aag tac ctc cgt gct gca aag aac ccc Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro 210 215 220			672
gtc atc ctt gtc gat gct tgt gct atc cgt cat cgt gtt ctt gat gag Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu 225 230 235 240			720
gtt cat gat ctc atc gaa aag aca aac ctc ccc gtc ttt gtc act cct Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro 245 250 255			768
atg ggc aaa ggt gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val 260 265 270			816
tat gcc ggt gac ggc tca cat ccg cct caa gtt aag gac atg gtt gag Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu 275 280 285			864
tct tct gat ttg ata ttg aca atc ggt gct ctc aag agc gac ttc aac Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn 290 295 300			912
act gct ggc ttc tct tac cgt acc tca cag ctg aac acg att gat cta Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu 305 310 315 320			960
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln 325 330 335			1008
atg agg ggt gtg ctg cga caa gtg att aag cag ctc gat gca tct gag Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu 340 345 350			1056
atc aac gct cag cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn 355 360 365			1104

cga gat aac tca ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg	1152
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val	
370 375 380	
gga gag ttc ctg aag aag aac gac atc gtc att acc gag act gga aca	1200
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr	
385 390 395 400	
gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg	1248
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala	
405 410 415	
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc	1296
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys	
420 425 430	
caa gga gcc gtt ctt gca gcc gcc gat gac aac agc gat cgc aga act	1344
Gln Gly Ala Val Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr	
435 440 445	
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg	1392
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu	
450 455 460	
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc	1440
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys	
465 470 475 480	
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag	1488
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu	
485 490 495	
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt	1536
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe	
500 505 510	
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag	1584
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu	
515 520 525	
ctg gac agc ctt ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc	1632
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu	
530 535 540	
cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg	1680
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu	
545 550 555 560	
atc atg acg gca gaa gct agc gcg agg aac aat gcc aag aca gag taa	1728
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *	
565 570 575	

<210> 19
<211> 575

<212> PRT
 <213> Unknown

<220>

<223> Fungal isolate from soil sample

<400> 19

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Val	Ala	Glu	Tyr	Leu	Phe	Arg	Arg	Leu	His	Glu	Ile	Gly	Ile	Arg	Ser
			20					25					30		
Ile	His	Gly	Leu	Pro	Gly	Asp	Tyr	Asn	Pro	Leu	Ala	Leu	Asp	Tyr	Leu
		35					40					45			
Pro	Ser	Cys	Gly	Leu	Arg	Trp	Val	Gly	Ser	Val	Asn	Glu	Leu	Asn	Ala
		50				55					60				
Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Val	Lys	Gln	Met	Gly	Ala	Leu
65				70						75					80
Ile	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala	Ile	Asn	Gly	Val	Ala
				85						90				95	
Gly	Ala	Phe	Ser	Glu	His	Val	Pro	Val	Val	His	Ile	Val	Gly	Cys	Pro
			100					105					110		
Ser	Thr	Ala	Ser	Gln	Arg	Asn	Gly	Met	Leu	Leu	His	His	Thr	Leu	Gly
		115					120					125			
Asn	Gly	Asp	Phe	Asn	Ile	Phe	Ala	Asn	Met	Ser	Ala	Gln	Ile	Ser	Cys
		130				135					140				
Glu	Val	Ala	Lys	Leu	Thr	Asn	Pro	Ala	Glu	Ile	Ala	Thr	Gln	Ile	Asp
145				150						155					160
His	Ala	Leu	Arg	Val	Cys	Phe	Ile	Arg	Ser	Arg	Pro	Val	Tyr	Ile	Met
			165					170						175	
Leu	Pro	Thr	Asp	Met	Val	Gln	Ala	Lys	Val	Glu	Gly	Ala	Arg	Leu	Lys
		180						185					190		
Glu	Pro	Ile	Asp	Leu	Ser	Glu	Pro	Pro	Asn	Asp	Pro	Glu	Lys	Glu	Ala
		195					200					205			
Tyr	Val	Val	Asp	Val	Val	Leu	Lys	Tyr	Leu	Arg	Ala	Ala	Lys	Asn	Pro
		210				215					220				
Val	Ile	Leu	Val	Asp	Ala	Cys	Ala	Ile	Arg	His	Arg	Val	Leu	Asp	Glu
225				230						235					240
Val	His	Asp	Leu	Ile	Glu	Lys	Thr	Asn	Leu	Pro	Val	Phe	Val	Thr	Pro
			245					250						255	
Met	Gly	Lys	Gly	Ala	Val	Asn	Glu	Glu	His	Pro	Thr	Tyr	Gly	Gly	Val
		260					265						270		
Tyr	Ala	Gly	Asp	Gly	Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu
		275					280					285			
Ser	Ser	Asp	Leu	Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn
		290				295					300				
Thr	Ala	Gly	Phe	Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu
305				310						315					320
His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln
			325					330					335		
Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu
		340						345					350		
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	
		355					360				365				
Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val
		370				375					380				
Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr
385				390						395					400

Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	
				405					410						415	
Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	
			420					425					430			
Gln	Gly	Ala	Val	Leu	Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	
		435					440					445				
Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	
	450					455					460					
Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	
465					470					475					480	
Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	
				485					490						495	
Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	
			500					505					510			
Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	
		515					520					525				
Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	
	530					535					540					
Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu	
545					550					555					560	
Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu		
				565					570					575		

<210> 20
 <211> 1728
 <212> DNA
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<221> CDS
 <222> (1)...(1728)

<400> 20																
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Met	Ala	Ser	Ile	Asn	Ile	Arg	Val	Gln	Asn	Leu	Glu	Gln	Pro	Met	Asp	
1				5					10					15		
gtt gcc gag tat ctt ttc cgg cgt ctc cac gaa atc ggc att cgc tcc																96
Val	Ala	Glu	Tyr	Leu	Phe	Arg	Arg	Leu	His	Glu	Ile	Gly	Ile	Arg	Ser	
			20					25					30			
atc cac ggt ctt cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg																144
Ile	His	Gly	Leu	Pro	Gly	Asp	Tyr	Asn	Leu	Leu	Ala	Leu	Asp	Tyr	Leu	
		35				40					45					
cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct																192
Pro	Ser	Cys	Gly	Leu	Arg	Trp	Val	Gly	Ser	Val	Asn	Glu	Leu	Asn	Ala	
		50				55					60					
gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc																240
Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Val	Lys	Gln	Met	Gly	Ala	Leu	
	65				70					75				80		
atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc																288

Ile	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala	Ile	Asn	Gly	Val	Ala		
				85					90					95			
ggt	gcc	ttt	tcg	gaa	cac	gtc	cca	gtc	ggt	cac	att	ggt	ggc	tgc	cct	336	
Gly	Ala	Phe	Ser	Glu	His	Val	Pro	Val	Val	His	Ile	Val	Gly	Cys	Pro		
			100					105					110				
tcc	act	gcc	tcg	cag	cga	aac	ggc	atg	ctc	ctc	cac	cac	acg	ctt	gga	384	
Ser	Thr	Ala	Ser	Gln	Arg	Asn	Gly	Met	Leu	Leu	His	His	Thr	Leu	Gly		
		115					120					125					
aac	ggc	gac	ttc	aac	atc	ttt	gcc	aac	atg	agc	gct	caa	atc	tct	tgc	432	
Asn	Gly	Asp	Phe	Asn	Ile	Phe	Ala	Asn	Met	Ser	Ala	Gln	Ile	Ser	Cys		
	130					135					140						
gaa	gtg	gcc	aag	ctc	acc	aac	cct	gcc	gaa	att	gcg	acc	cag	atc	gac	480	
Glu	Val	Ala	Lys	Leu	Thr	Asn	Pro	Ala	Glu	Ile	Ala	Thr	Gln	Ile	Asp		
	145				150					155					160		
cat	gcc	ctc	cgc	gtt	tgc	ttc	att	cgt	tct	cgg	ccc	gtc	tac	atc	atg	528	
His	Ala	Leu	Arg	Val	Cys	Phe	Ile	Arg	Ser	Arg	Pro	Val	Tyr	Ile	Met		
			165					170						175			
ctt	ccc	acc	gat	atg	gtc	cag	gcc	aaa	gta	gaa	ggt	gcc	aga	ctc	aag	576	
Leu	Pro	Thr	Asp	Met	Val	Gln	Ala	Lys	Val	Glu	Gly	Ala	Arg	Leu	Lys		
			180					185					190				
gaa	cca	att	gac	ttg	tcg	gag	cct	cca	aat	gat	ccc	gag	aaa	gaa	gca	624	
Glu	Pro	Ile	Asp	Leu	Ser	Glu	Pro	Pro	Asn	Asp	Pro	Glu	Lys	Glu	Ala		
		195					200					205					
tac	gtc	gtt	gac	gtt	gtc	ctc	aag	tac	ctc	cgt	gct	gca	aag	aac	ccc	672	
Tyr	Val	Val	Asp	Val	Val	Leu	Lys	Tyr	Leu	Arg	Ala	Ala	Lys	Asn	Pro		
	210					215					220						
gtc	atc	ctt	gtc	gat	gct	tgt	gct	atc	cgt	cat	cgt	gtt	ctt	gat	gag	720	
Val	Ile	Leu	Val	Asp	Ala	Cys	Ala	Ile	Arg	His	Arg	Val	Leu	Asp	Glu		
	225				230				235					240			
gtt	cat	gat	ctc	atc	gaa	aag	aca	aac	ctc	ccc	gtc	ttt	gtc	act	cct	768	
Val	His	Asp	Leu	Ile	Glu	Lys	Thr	Asn	Leu	Pro	Val	Phe	Val	Thr	Pro		
			245					250						255			
atg	ggc	aaa	ggt	gct	gtt	aac	gaa	gaa	cac	ccg	aca	tat	ggt	ggt	gtc	816	
Met	Gly	Lys	Gly	Ala	Val	Asn	Glu	Glu	His	Pro	Thr	Tyr	Gly	Gly	Val		
			260					265					270				
tat	gcc	ggt	gac	ggc	tca	cat	ccg	cct	caa	gtt	aag	gac	atg	gtt	gag	864	
Tyr	Ala	Gly	Asp	Gly	Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu		
		275					280					285					
tct	tct	gat	ttg	ata	ttg	aca	atc	ggt	gct	ctc	aag	agc	gac	ttc	aac	912	
Ser	Ser	Asp	Leu	Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn		
	290					295					300						
act	gct	ggc	ttc	tct	tac	cgt	acc	tca	cag	ctg	aac	acg	att	gat	cta	960	
Thr	Ala	Gly	Phe	Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu		

305	310	315	320	
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag				1008
His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln				
325		330	335	
atg agg ggt gtg ctg cga caa gtg att aag cag ctc gat gca tct gag				1056
Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu				
340		345	350	
atc aac gct cag cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac				1104
Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn				
355		360	365	
cga gat aac tca ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg				1152
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val				
370		375	380	
gga gag ttc ctg aag aag aac gac atc gtc att acc gag act gga aca				1200
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr				
385		390	395	400
gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg				1248
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala				
405		410	415	
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc				1296
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys				
420		425	430	
caa gga gcc gtt ctt gca gcc gcc gat gac aac agc gat cgc aga act				1344
Gln Gly Ala Val Leu Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr				
435		440	445	
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg				1392
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu				
450		455	460	
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc				1440
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys				
465		470	475	480
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag				1488
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu				
485		490	495	
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt				1536
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe				
500		505	510	
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag				1584
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu				
515		520	525	
ctg gac agc ctt ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc				1632
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu				
530		535	540	

cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg 1680
 Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu
 545 550 555 560

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 35 40 45
 Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
 50 55 60
 Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
 65 70 75 80
 Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
 85 90 95
 Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
 100 105 110
 Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
 115 120 125
 Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
 130 135 140
 Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
 145 150 155 160
 His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met
 165 170 175
 Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys
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 Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala
 195 200 205
 Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro
 210 215 220
 Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu
 225 230 235 240
 Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro
 245 250 255
 Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val
 260 265 270
 Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu
 275 280 285
 Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn

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His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln
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Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu
			340						345					350	
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn
		355							360					365	
Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val
		370							375					380	
Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr
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Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala
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Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys
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Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe
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Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu
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		530							535					540	
Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu
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Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu	
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